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SOURCE Dunio rerio (zebrafish) REFERRICE ALTINGCTHESPI (SPETINGER) DUNIO. REFERRICE (PAPINIATION DUNION) S.L. LAHRAH, H. Dee, R. L. JF., MARITAN, BECK.C., WALIS.T. PRESENCE (PAPINIATION DUNION) S.L. LAHRAH, H. Dee, R. L. JF. MARITAN, B. DOWERT, S. HILLISTI Nuchae, T. MARTING, B. ALTINIATI Nuchae, T. MARTING, B. ALTINIATI Nuchae, T. MARTINIA, B. DOWER, N. SCHALK, R. MARTENEON, R. and Milson, R. Jackson, Y., Cardenas, M., McCann, R., MARTENEON, R. and Milson, R. Jackson, Y., Cardenas, M., McCann, R., MARTENEON, R. and Milson, R. Jackson, Y., Cardenas, M., McCann, R., Attanania Contact: Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Johnson WARNINGTON University School of Medicine General Contact: Stephen L. Johnson MARITAN ENGRAPH CONTACT CONT	Query Match 42.6%; Score 16.2; DB 1; Length 46; Rest Local Similarity 72.4%; Pred. No. 1.18+05; Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0; Qy 1 GGGGACTTTCCGGGGGG 29
AUJOGSSO AUJ	AI544460 fb75b10.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3717691 3' similar to SW:CA19 HUMAN P20849 COLLAGEN ALPHA 1(RX) CHAIN PRECURSOR. ;, mRNA sequence. AI544460 AI544460.1 GI:4461833 EST.
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- Charles L. L.

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Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Bay Area Functional Genomics Consortium (BayGenomics)
Bay Area Functional Genomics.ucsf.edu
Benail: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
Gell line. ES call lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
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Class: Gene Trap.
Location/Qualifiers
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:82-42-866-7181, Fax:82-42-860-4409) Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance PRIMERS
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RST325 BayGenomics Gene Trap Library pGT2TMpfa Mus musculus cDNA,
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Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 49)
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Pred. No. 1.4e+05;
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Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
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Pan troglodytes DNA, clone: RP43-079M17.T7, genomic survey
sequence.
                                                       AA878803 CGAP Li5 Homo sapiens cDNA clone IMAGE:1437246 3' similar to SW:PRPM FUDMA PI0161 SALIVARY PROLINE-RICH PROTEIN PO ; contains TAR1.t3 TAR1 repetitive element ;, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                              Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished
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Unpublished (1997)
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Email: cgapbs-r@mail.nih.gov
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Trace considered overall poor quality
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High quality sequence stop: 1.
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/tissue_type="hepatic adenoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 CCGCTGGGGACTTTCCAGGGGGAC 33
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                                                                                                                                                                       AA878803.1 GI:2987768
                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                  Homo sapiens
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Best Local Similarity
Matches 19; Conserv
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                   RESULT 2
AA878803/c
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AG198773/c
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6 CTTTCCGCTGGGGACTTTCCAG 27
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                                                                                 RESULT 6
AI416657
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1MAGE:158876 5' similar to SP:A42445 A42445 FSP27=FAT-SPECIFIC GENE
FSP27 - ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 716
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 716 Std Brror: 0.00
Seq primer: MIJRP;
High quality sequence stop: 1.
High quality sequence stop: 1.
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1 (bases 1 to 37)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Indels
 5
0; Mismatches
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/mol_type="mRNA"
/db_xref="GDB:572930"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:158876"
/sex="Female"
                                 4 GACTITCCGCTGGGGACTITCCAG 27
                                                               26 GACTTTCCGCTGGGGTGTCACCCG 3
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                   R75772
R75772.1 GI:850454
19; Conservative
                                                                                                                                                                                                                                                                      SOURCE
ORGANISM
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Matches
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JOURNAL
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                                                                                                                  RESULT 5
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Gaps

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41.1%; Score 15.6; DB 8; llarity 81.8%; Pred. No. 1.9e+05; Conservative 0; Mismatches 4;

Query Match Best Local Similarity Matches 18; Conserv

Length 37; Indels

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/clone lib="Gar-Cloos"
//note="Wetcor: pBluescript II XR; Site 1: ECORI; Site 2:
Xhoi; Immature Cotyledon CDNA. The mRNA was isolated and
then Stratagene's CDNA Synthesis Kit (catalog #200401) was
used to synthesize the CDNA. First-strand synthesis was
performed with 5-methyl dCTP, hence the ligated CDNA is
heminethylated. Stratagene's first-strand synthesis primer
was used (GAGAGAGAGAGACATAGTCTGGAG(T)-18]. After
second-strand synthesis, the CDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by dispestion with XhoI;
all XhoI sites in the CDNA would be protected by their
hemimethylated status. The CDNA constructs were
size-fractionated with a SOODp cutoff, using GibcoBRL Life
Technologie s' CDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+) that had been
                                                                                                                                                                                                   28 bp mRNA linear EST 23-JUL-2004 sal0bb4.xl Gm-c1003 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1003-8 3' similar to WP:W03D2.1 CE14506 ;, mRNA sequence. AI416657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khamn, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Sowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Public Soybean EST Project
Unpublished (1999)
Other ESTS: salobol, Yublic Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watcon.wustl.edu
When it has been determined, an EST from the other end of this
When it has been determined, an clone' field. Other ESTs:
salobo4.yl GENOWE SYSTEMS CLONE ID: Gm.-cl003.8 Trace considered
overall poor quality Possible reversed clone: similarity on wrong
strand This clone is available through: Biogenetic Services, 801
32nd Ave. Brookings, 20 57006 USA (phone: 800 423 4163; email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/clone="GRNOME SYSTEMS CLONE ID: G
/tissue_type="immature cotyledon"
/lab_host="XLl0-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Glycine max"
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/cultivar="Williams"
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                    24
3 CTTTCCGCTGGGCCCTCTTCAG
                                                                                                                                                                                                                                                                                                                                                                           AI416657.1 GI:4260161
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Gaps

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muscular colours DNR Resource (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil | 4732114 | gb| | kb129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wen. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                           GSS 16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Guirognathi; Muroidea; Muridae; Murinae; Mus.

1 (Dases 1 to 34)

1 (Dases 1 to 34)

1 Islam, H., Longacre, S., Mahmod, M., Meenen, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Niederhausern, A. and Wright, D., Weiss, R.

Plasmid inserts

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                     AZ760788 16-FEB-200 1MO554F14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0554F14 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/close_lib="Mouse_10kb plasmid UUGCNM library"
/note="Wector: PWD4Zlv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                Length 34;
                                                                                                                                  Indels
        Bento Soares and M. Fatima Bonaldo.
                                                                             Score 15.4; DB 1;
Pred. No. 2.2e+05;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: F column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
                                                                                                                                                                                         6 crircccricccarriccaccecacciric 38
                                                                                                                                                                                                                        /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0554F14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ760788.1 GI:12869009
                                                                                Query Match
Best Local Similarity 66.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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SOURCE
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AZ760788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NG-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1357237

A1357237

A1357237

A25308.X1 NCI CGAP GC4 HOMO sapient cDNs clone IMAGE:2006006 3'
asimilar to SW:PRP2 HUWAN PO2812 SALIVARY PROLINE-RICH PROTEIN
PRECURSOR ;contains element MSR1 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 34)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                               Query Match 40.5%; Score 15.4; DB 1; Length 28; Best Local Similarity 76.0%; Pred. No. 2.2e+05; Matches 19; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                    University of Illinois"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TTTCCGCTGGGGACTTTCCAGGGGG 31
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Homo sapiens
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Class: transposon-tagged
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GSS.
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AI917121.1 GI:5636976
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                                                                                                                                                  survey sequence.
CG776618
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/cultivar="mixed background W23/A188/B73"
/tifsue_type="leaf"
/tifsue_type="leaf"
/dev stage="leaf"
/dev sta
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1 (bases 1 to 50)
Walbot, V.
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford University
855 California Ave, Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 8221
Email: walbot@stanford.edu
Email: walbot@stanford.edu
Reverse complemented post-ligation sequence from source sequence.
Plate: 1118010 row: 20
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                                                                                                                        Query Match 40.5%; Score 15.4; DB 9; Length 34; Best Local Similarity 76.0%; Pred. No. 2.2e+05; Matches 19; Conservative 0; Mismatches 6; Indels
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/dev stage="adult"
//dev stage="adult"
//dev stage="adult"
//deb_host="pH108"
//clone_lib="1123 - RescueMu Grid L"
//note="Organ: leaf; Vector: RescueMu (engineered from note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units: Por more information on RescueMu, go to the web site 'www.zamdb.iastate.edu' and follow the links for secueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B colls were transformed and then screened on LB plates with
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ts52a12.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:2232190 3' similar to SW:CA13 EOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN.
contains element TAR1 repetitive element; , mRNA sequence.
CG776618 42 bp DNA linear GSS 29-OCT-2003
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Contact: Walbot V
Department of Biological Sciences
Stanford University
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Sposible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1123002 row: 2
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/culfivar="mixed background W23/A188/B73/K55"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227
Fax: 650 725 8221
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こち 大学行情

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CL878011 38 bp DNA linear GSS 30-AUG-2004 abf23b12.x1 Soybean random, unfiltered genomic library Glycine max
Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                       /clone_"CAS09420"
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/dlone="MSDE001650"
/clone_lib="Sugano Homo sapiens cDNA library"
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                     Length 50;
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Pred. No. 4.7e+05;
0; Mismatches 9;
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                                                             Location/Qualifiers
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69.0%;
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|/organism="Homo sapiens"
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|/mol_type="mRNA"
|/db_xref="taxon:9606"
|/clone="INAGE:223190"
|/tissue_type="renal cell tumor"
|/db_hogf="DH10B"
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|/db_hogf="mroi CGAP Kid8"
|/dote="organ: kidas"
|/note="organ: kidas"
|/note="organ: kidas"
|/note="organ: kidas"
|/note="organ: kidas"
|/note="organ: kidas"
|/note="organ: kidas: disport size 1.2 kb. Life Technologies catalog #:
                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.,
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E., Consortium/LLNL at:
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae, Forman, meaturoutugiires; Frimates; Catarrhini, 1 (bases Homo.

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Sakuki,Y., Taora,H., Tsunoda,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale EMBO Rep. 2 (5), 388-393 (2001)
                                               Hominidae, Homo.
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.4%; Score 14.6; DB 1; Length 46; llarity 69.0%; Pred. No. 4.7e+05; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ww-bio.llnI.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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Unpublished (1997)
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/organism="Mus musculus"
/mol type="genomic DNA"
/brain="c57BL/60"
/db xref="taxon:10090"
/clone="UUGCIM0080K22"
                                                                                                                                                                               /mol_type="genomic_DNA"
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 45.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
/cultivar="Williams 82"
/cultivar="Williams 82"
/chore_type="Young leaves"
/clone_lib="Soybean random, unfiltered genomic library"
/note="Vector: pOT2; Site 1: BstX1; Randomly sheared
/note="Vector: pOT2; Site 1: BstX1; Randomly sheared
/note="Vector: pOT2; Site 1: BstX1; Randomly sheared
/note="Vector: pOT2; Site 1: BstX1; Cout poT2. LibID: 230"
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Wagnoliophyta; eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.

(bases 1 to 42)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shimn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                 Eufaryona, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and
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                                                                                                                                                                                                                                                                                  Methylation filtered genomic sequences from Glycine max Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
1010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                          Contact: Gary Stacey
University of Missouri
University of Columbia, MO 65211, USA
Tel: 573-884-1267
Fax: 573-882-0588
genomic, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Smail: staceyg@missouri.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burvey sequence.
BZ288740
BZ288740.1 GI:24329178
                   CL878011.1 GI:51610429 GSS.
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Class: shotgun.
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nes 15; Conserv
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AA2345648 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080K22 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                  /db xref="taxon:3702"
/clone="SALK_02130.29.10.x"
/clone="SALK_02130.29.10.x"
/clone="lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At5g17610.
Class: TDNA tagged.
Location/Qualifiers
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Dunn,D., Acyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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0
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    42
/organism="Arabidopsis thaliana"

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Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: K column: 22
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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50 bp mRNA linear EST 28-JAN-2004
AU106577 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT03453, mRNA sequence.
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Smail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a S.-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

Hominidae, Homo.

Lobaes 1 to 50.

Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mana start sites

EMBO Rep. 2 (5), 388-393 (2001)
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/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                Length 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.4; DB 1;
Pred. No. 5.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ACTITCCGCTGGGGACTITCCAGG 28
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                                                                                                                                                                                                                                                                                                                                                                                                                   37.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 75.0
hes 18; Conservative
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Best Local Similarity
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ORGANISM
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                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwalvel (gill 4732114 [gb] AR12972.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nib.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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Mukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
I Chaese I to 40
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aa59c05.rl NCI CGAP GCB1 Homo sapiens cDNA linear EST 18-AUG-1. similar to SW:YET7 YEAST P40066 HYPOTHETICAL 40.5 KD PROTEIN IN NUPL57-SW14 INTERGENIC REGION. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%; Score 14.4; DB 9; Length 45; larity 75.0%; Pred. No. 5.6e+05; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:825224"
/tissue_type="germinal center B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 GCTGGGGACTTTCCAGGGGACTT 35
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Unpublished (1997)
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Matches 18; Conserv
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone_Ibb="HIV-vector integration sites from
/clone_Ibb="HIV-vector integration sites from
/clone_Ibb="HIV-vector integration sites from
/clone_Ibb="HIV-vector integration sites from
/clone_Ibb="HIV-vector integration integrated by the sequences in noncoding human DNA
that are associated with repression of an integrated human
immunodeficiency virus type 1 (HIV-1) promoter. HIV-1
integration results in the formation of precise and
homogeneous junctions between viral and host DNA, but
integration takes place at many locations. Thus, the
variation in HIV-1 gene expression at different
integration takes procest the activity of regulatory
sequences at nearby chromosomal positions. Negative
regulation of HIV transcription is of particular interest
because of its association with maintaining HIV in a
latent state in cells from infected patients. To identify
chromosomal regulators of HIV transcription, we infected
Jurkat T cells with an HIV-based vector transducing green
fluorescent protein (GFP) and separated cells into
populations containing well-expressed (GFP-positive) or
populations containing well-expressed (GFP-positive) or
populations containing well-expressed (GFP-positive)
sequencing 971 junctions between viral and cellular by
Possbible effects of endogenous cellular transcription were
characterized by transcriptional profiling. Low-level GFP
expression correlated with integration in (i) gene
deserved.
                                                                     GSS 07-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.

I (bases 1 to 3):

Lewinski, M.K., Bisgrove, D., Shinn, P., Chen, H., Hoffmann, C.,

Hannenhalli, S., Verdin, B., Berry, C.C., Ecker, J.R. and Bushman, F.D.

Genome-wide analysis of chromosomal features repressing human

immunodeficiency virus transcription

J. Virol. 79 (11), 6610-6619 (2005)

15890899
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                  CZ442924

1B35002.fwd HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells Homo sapiens genomic clone IBB3002.fwd, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Microbiology
University of Pennsylvania School of Medicine
402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bushman@mail.med.upenn.edu
Class: PCR with specific primers.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                          CZ442924.1 GI:62379025
                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Bushman FD
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Fax: 215 573 4856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19104-6076, USA
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                              LOCUS
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KEYWORDS
SOURCE
ORGANISM
RESULT 19
CZ442924/c
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COMMENT
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A1039253

40 bp mRNA linear EST 28-AUG-1998
0x33b01.81 Scares total fetus Nb2HF8 9w Homo sapiens cDNA clone
IMAGE.1658089 3' similar to SW:PF11_FIG P51524 PROPHENIN-1
PRECURSOR ;, mRNA sequence.
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                                                                                                                                                         GSS 13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TREU927/4 GUTAL 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Maxing small
insert libraries for whole genome shorgun sequencing projects. In
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrell, Oxford University Press, 1999).
Email: nelsayed@rigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.nkProjects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campus, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                37 bp DNA linear GSS 13-DE
T. brucei sheared genomic DNA clone 379b06, reverse sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hir Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 6.4e+05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Trypanosoma brucei"
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strain="TREU927"
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GCTGGGGACTTTCCAGGGGGACTTTCC 38
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                          27 GGTGAGTACTCTGCAGGAGGACGTTAC 1
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70.4%;
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Trypanosoma brucei
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(bases 1 to 37)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nhl@sanger.ac.uk
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AUTHORS

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Gaps

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Score 14.2; DB 10; Length 35; Pred. No. 6.4e+05; 0; Mismatches 8; Indels

Query Match 37.4%; Best Local Similarity 70.4%; Matches 19; Conservative (

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CC459460 50 bp DNA linear GSS 30-MAY-2003 SALK 129954.28.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_129954.28.55.x, genomic
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/db xrefe="cxxon:3702"
/clone="SALK 12954.28.55.x"
/clone libe-Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
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adatrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is single pass sequence recovered from the left border of
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                                                             /clone="ADSE00150"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                            Length 50;
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fle: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 50;
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Pred. No. 6.7e+05;
0; Mismatches 8;
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/mol_type="genomic DNA"
/ecotype="Col-0"
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Pred. No. 6.7e+05;
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  organism="Homo sapiens"
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                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADSE00350"
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Location/Qualifiers
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                                                                                                                                            Query Match 37.4%;
Best Local Similarity 70.4%;
Matches 19; Conservative
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Unpublished (2001)
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                                                                                                                                                                                                                                                                                 Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ima.u-ckyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1199-156 (1997).
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AU104208 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoffa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 50)
Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA scart sites
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1067 Std Error: 0.00
Seq primer: -40413 fwd. Err from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by Bento Soares and M. Fatima Bonaldo. "
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/organism="Homo sapiens"
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AU104208
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Homo sapiens
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AU104208/c
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/clone='IndGE:1571509"
/tissue_type="pooled germ cell tumors"
/tissue_type="pooled germ cell tumors"
/lab_hote="blublubs"
/clone lib="NCI CGAP GC4"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylimer; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
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Pan troglodytes DNA, clone: RP43-065002.TJ, genomic survey
sequence.
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                                                                                                                                                                                                                                                                           Sequencing Center
information can be
                                                                                                                              Email: cgapbs.romail.min.gov
Trisue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AG190424.1 GI:45222600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-0CT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evy cedex, FRANCE
Gaston Cremieux, 91057 Evy cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versaillee). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at thtp://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (Rittp://www.genoplante.com and http://genoplante-info.infoiogen.fr).

Location/Qualifiers
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                         AJS87887 50 bp DNA linear GSS 15-JAN-2004
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                           Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                          336H01, genomic survey sequence.
AJ597887.
AJ597887.1 GI:37937511
GSS, left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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left border"
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Homo sapiens
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1 (bases 1 to 34)
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AA931137/c
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilfa732114 [gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Tel: 801 585 5606
Fax: 801 585 7177
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1 (bases 1 to 40)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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1M0545P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0545P18 F, genomic survey sequence.
     /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0545 row: P column: 18
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0545P18"
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Mus musculus
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Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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1 (bases 1 to 40)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rally, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Under Genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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Fax: 801 585 7177
Email: ddunn@enetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0408 row: O column: 08
Seg primer: CACAACAGGAAACAGGTATGACC
Class: plasmid ends
High quality sequence stop: 40.
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/bb xref="taxon:9598"
/clone="RP43-065002.TJ"
/sex="male"
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/organism="Mus musculus"
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0408008"
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                    : pBACe3.6
: EcoRI
: EcoRI.
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                                                                                                                  Sequencing: TJ
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R.Site 2
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AZ595836
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Gaps ; GSS 14-DEC-2000

organism="Drosophila melanogaster"

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                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114[gb]AR129072.1); a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Ephydroidea; Drosophildae; Drosophila.

[Lobase 1 to 40]

Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.H. L., Ryner, L., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Lanfer, A., Mazzotta, J., Smith, R.D., Stevens L.M., Stuber, C., Tan, L.R., Ventura, W., Woo, A., Zakrajsek, L., Zhao, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L., and Margolis, J. A. complementary transposon tool kit for Drosophila melanogaster
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
//note="Wector: PWD42rv; Purified genomic DNA from M.
musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L248/95/
f05395-3prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic Sequence recovered from 3' end of piggyBac,
genomic survey sequence.
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Sequence orientation is forward strand relative to 5' end of piggyBac element.
The piggyBac element.
The piggyBac insertion position is 1 in the 40 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
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CZ487957.1 GI:62985395
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14981521
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CZ487957
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/downers the "Exelixa piggyBac WH insertions"
//donellb="Exelixa piggyBac WH (GenBank accession number
//note="Vector: piggyBac WH (GenBank accession number
AY515148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin:piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsinscy balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."
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Bay Area Functional Genomics Consortium (BayGenomics)
Bmail: infoobaygenomics.ucsf.edu
Sequence tag generated by S. RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
CELL_LINE&KEY=XG205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC200179 41 bp mRNA linear GSS 09-MAY-2003
XG205 BayGenomics Gene Trap Library pGT1Lxf Mus musculus CDNA, mRNA
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
1 (bases 1 to 41)
BayGenomics.
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/note="Vector: pGT1Lxf"
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Pred. No. 7.8e+05;
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Pred. No. 7.8e+05;
Taranes 5; Indels
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/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                  36.7%; Scor. 66.7%; Pred. No. ,..
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/sex="Male"
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Location/Qualifiers
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Unpublished (2001)
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/strain="129 ola"
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Mus musculus
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/clone="INAGE:1466028"
/lab_host="DH10B"
/clone="Cosares"
/clone="InAGE:1466028"
/clone="Organ: pooled: Vector: pT773D-Pac (Pharmacia) with
/note="Organ: pooled: Vector: pT773D-Pac (Pharmacia) with
/note="Organ: pooled: Vector: pT773D-Pac (Pharmacia) with
gqual amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_CGAP_GCB1) were mixed, and so circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731339. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A1357381 49 bp mRNA linear EST 15-FEB-1999 qy13b05.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2011857 3' similar to TR:Q15214 Q15214 SALIVARY PROLINE-RICH PROTEIN 1 ;contains element MSR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 49)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI/ONDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gen Index.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
1 (bases 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAIJONAl Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 790 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
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                                                                                                                         45 bp mRNA linear GSS 22-MAR-2005
G076G08 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
CL640557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U3CEO gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at: 'http://genetrap.gsf.de/project/web new/database/result_clone.html?' clone id=G076G08' ES cell line harboring insertion mutation of target gene is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 20122
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Sukarycha, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/cell_line="ES cells [C57BL/6J x 12986/SvEvTac] Fl"
/clone_lib="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Mar 22, 2005 this sequence version replaced gi:49489004.
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A46 bp mRNA linear EST 04
A448405.81 Soares NFL TGBC S1 Homo sapiens CNNA clone
IMAGE:1460528 3' similar to SW:PRP1 HUMAN P04280 SALIVARY
PROLINE-RICH PROTEIN PRECURSOR ;, mRNA sequence.
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/strain="129 Sv"
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German Genetrap Consortium (GGTC)
Email: info@genetrap.de
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/clone="G076G08"
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     26 GATATICCICTIGGGICTITIC 5
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Mus musculus
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AI432930.1 GI:4285621
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Best Local Similarity 72.0%
Matches 18; Conservative
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A1432930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Right at:
http://image.llnl.gov
High quality sequence start: 3
High quality sequence start: 3
High quality sequence stop: 50.
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Clone distribution: NCI-CGAP clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIH-MGC http://mgc/nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 36.8%; Score 14; DB 1; Length 49; Similarity 60.5%; Pred. No. 8e+05; 23; Conservative 0; Mismatches 15; Indels
                 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clonne="IMAGE:2011857"
/lissue_type="qlioblastoma (pooled)"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 GGGTTTTTTCCCTTTTTTGGGGGTTTTTCC 2
                                                                    Trace considered overall poor quality Insert Length: 672 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence scop: 1. Location/Qualifiers
                                                                                                                                                                    1. .49
/organism="Homo sapiens"
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/strain="FVB/N"
/db_xref="taxon:1
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Matches 23; Conserv
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AUTHORS
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BE311372
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Hominidae, Homo.

1 (bases 1 to 28)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015

DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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28 bp mRNA linear EST 13-APR-1999
th44C11.x1 NCI CGAP Lyml2 Homo sapiens CDNA clone IMAGE:2121140 3'
similar to SW:FRP2 HUMAN PO2812 SALIVARY PROLINE-RICH PROTEIN
PRECURSOR ; contains element MSR1 repetitive element ;, mRNA
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5" months"
/lab_host="DHIDB"
/lab_host="DHIDB"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
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/clone lib="NCI CGAP Lyml2"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sal1; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 8.8e+05;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                     Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                     36.8%; Score 14; DB 2; 77.3%; Pred. No. 8e+05; ative 0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/mol type="manual"
/mol type="manual"
/mol type="manual"
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/db xref="taxon:960"
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adenocarcinoma, 7 pooled tumors"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
                                                                                                                                                                  AI579983

tq45a05.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2211728 3'
similar to TR:Q08805 Q08805 SALIVARY PROLINE-RICH PROTEIN L
jcontains element MSR1 repetitive element j, mRNA sequence.
AI579983
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Danio rerio genomic clone DKEY-48J2, genomic survey sequence.
AL982948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washingron University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trace considered overall poor quality Insert Length: 2882 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 1 POLYA-No.
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  TCCGCTGGGGACTTTCCAGGGGGAC 33
                                                    9 rcccardedeargraaadedeaac 33
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Best Local Similarity
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DR48J2S/c
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                                                                                                                                                                     GSS 13-DEC-2000
                                                                                                                                                                  AZ628058 33 bp DNA linear GSS 13-DEC-200
1M0476122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0476122 F, genomic survey sequence.
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: I column: 22
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Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Nm. 308, Blomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0476122"
GGGGAATTTCCCCGGGGCCCCCC 25
                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                             AZ628058.1 GI:11750248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l. .33
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AUTHORS
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TITLE

COMMENT

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Gaps . 0

AL982948.1 GI:25186174 GSS. Danio rerio (zebrafish)

VERSION KEYWORDS SOURCE

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36.3%; Score 13.8; DB 9; Length 33; ilarity 72.0%; Pred. No. 9e+05; Conservative 0; Mismatches 7; Indels

Query Match Best Local Similarity Matches 18; Conserv

ORGANISM

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A1223998
46 bp mRNA linear EST 21-DEC-1998 qx125h07.x1 NCI CGAP Lyml2 Homo sapiens cDNA clone landEs:2001181 3' similar to TR:Q04154 Q04154 SALIVARY EROLINE-RICH PROTEIN RP15 PRECURSOR. ;contains element MER22 repetitive element; mRNA
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
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/note="Togan: lymph node; Vector: pCMV-SPORT6; Site_1:
Sal; Site_2: Not!; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (Dases 1 to 46)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
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£D/5bl0.xl Zebrafish WashU MPIMG EST Danio rerio CDNA clone
IMAGE.3717691 3' similar to SW:CA19 HUMAN P20849 COLLAGEN ALPHA
1(IX) CHAIN PRECURSOR.;, mRNA sequence.
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Pred. No. 9.4e+05;
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63.6%; Pred. No. 9.5e+05;
iive 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Confeact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 1534 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
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                                                                                                  36.3%; Scor.
88.2%; Pred. No. >...
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    .46
    /organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:2001181"
                                                                                                                                                                                                           15 GGGGACTTTCCAGGGGG 31
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AI223998/c
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                                                                                                                                                  Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hunguery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 48J2. 48J2 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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43 bp mRNA linear EST 13-APR-1999 ti06c03.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2129668 3' similar to TR:000599 000599 CON1. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cyriniformes, Cyprinidae, Danio.

1 (bases 1 to 41)

Humphray, S.J., Huckle, E. and Hunt, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 43)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                  Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 41;
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Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                    1. 41
Aorganism="Danio rerio"
Amol type="genomic DNA"
Ab_xref="taxon:7955"
Aclone="DKBY-4812"
/tissue type="Testis"
/note="yector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Insert Length: 1286 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2129668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 CGCTGGGGACTTTCCAGGGGGACTT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 cccerccirirccccccrrcir 16
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AI520679.1 GI:4434814
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Homo sapiens
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
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Best Local Similarity
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AIS20679/c
LOCUS
DEFINITION
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ORGANISM
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AUTHORS
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TITLE
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KEYWORDS
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us-09-669-187a-148szlm50.rst

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BJ057570 Hibb Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL104h07 5', mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="stage 25" /clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
                                                                                                                                                                                                                                                                                                                                Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.3%; Score 13.8; DB 3; Length 46; 66.7%; Pred. No. 9.5e+05; Live 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Conteat: Tadamu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole embryo"
                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                               Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Xenopus laevis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL104h07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshinisgenes.nig.ac.jp
The information of this clone
URL.
                                                                                                                                                                                                                                                                                             Kenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                                                                                                                                                                 BJ057570.1 GI:17479651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111 Yata, Mishima,
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                               (bases 1 to 46)
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KEYWORDS
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                                          RESULT 42
                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                           BJ057570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Mashington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cypriniformes; Cyprinidae; Danio.

E 1 (bases 1 to 46)
S Clark, Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Skaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Unpublished (1998)
L. Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: T7 ET from Amersham
High quality sequence stop: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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Pred. No. 9.5e+05;
0; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /orqanism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="IMAGE:3717691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                      EST.
Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.3%;
AI544460.1 GI:4461833
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Best Local S:
Matches 21,
                                                                ORGANISM
                                                                                                                                                  REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
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EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL

COMMENT

TITLE

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Gaps ö

Indels

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21; Conservative

11375929 Contact: Yutaka Suzuki

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BH812215 32 bp DNA linear GSS 02-MAY-2002 SALK 061414 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_061414, genomic survey sequence.
                                                                    CRI78464 S0 bp DNA linear GSS 06-JUL-2004 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP340e12, genomic survey sequence. CRI78464
                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1. (bases 1 to 50)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Birect Submission
Submitted (20-FRB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
dadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaрв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.3%; Score 13.8; DB 11; ilarity 88.2%; Pred. No. 9.6e+05; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana"
                                                                                                                                                                            CR178464.1 GI:49957313
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .50
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPP340e12"
/clone_lib="MHPP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="genomic DNA"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 GCTGGCGACATTCCAGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 32)
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KEYWORDS
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SOURCE
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                                         RESULT 45
CR178464/c
LOCUS
                                                                                                            DEFINITION
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Matches
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K.; Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
1-ength-enriched and a S'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
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Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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I (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)
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                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/mol_traxon:9606"
/clone="HRP22967"
/clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="txxon:9606"
/db_cref="txxon:9606"
/clone="LM013032"
/clone_lib="Sugano Homo sapiens cDNA library"
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36.3%; Score 13.8; DB 1;
Best Local Similarity 63.6%; Pred. No. 9.6e+05;
Matches 21; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.8; DB 1;
Pred. No. 9.6e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CTTTCCGCTCGGCTGTTTCCTGCGCAGGTTTC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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1 Similarity 63.6%;
21; Conservative
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DEFINITION
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU327/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Orwond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Direct Submission
Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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T. brucei sheared genomic DNA clone 26H11, reverse sequence,
genomic survey sequence.
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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Best Local Similarity 67.9%; Pred. No. 1.1e+06;
Matches 19; Conservative 0; Mismatches 9;
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35.8%; Score 13.6; DB 9;
Best Local Similarity 67.9%; Pred. No. 1.1e+06;
Matches 19; Conservative 0; Mismatches 9;
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/strain="TREU927"
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                               /db xref="taxxn:3702"
/clone="SALK 06144"
/clone="SALK 06144"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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2M0007G07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0007G07 R, genomic survey sequence.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/clone_llb="Mouse_lokb plasmid UUCCN library"
/note="Vector: PWB4Zlv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1.0.40)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.8%; Score 13.6; DB 9; Length 32; 80.0%; Pred. No. 1.1e+06;
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Fax: 801 585 7177
Bmail: ddunmgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0007 row: G column: 07
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0007G07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 40.
Location/Qualifiers
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Mus musculus
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84112, USA
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Best Local Simi
Matches 16;
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KEYWORDS
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Search completed: February 15, 2006, 21:10:37 Job time : 2541.47 secs
Homo sapiens (human)
SOURCE
ORGANISM
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                                                                                       REFERENCE
AUTHORS
TITLE
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S Marra, M. Hillier, L. Allen, M. Bowles, M. Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Waleing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. The WashU-HMI Mouse EST Project

I Unpublished (1956)

Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 bp mRNA linear EST 01-OCT-1997
ma41b12.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:313247 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI635210 46 bp mRNA linear BST 16-DEC-1999 tz22e06.xl NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2289346 3' similar to SW:EXIN_DAUCA P06599 EXTENSIN PRECURSOR. ;, mRNA
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                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                            Mus musculus (house mouse)
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AI635210
AI635210.1 GI:4686540
EST.
                                                                                                          W10989.1 GI:1285294
                                                                                                                                                               Mus musculus
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                                                   DEFINITION
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AI635210/c
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VERSION
KEYWORDS
 RESULT 49
W10989/c
                                                                                         ACCESSION
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KEYWORDS
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Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NII-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH108"
/clone lib="NCI_CGAP_Ut2"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Homoinidae; Homo.

1 (bases 1 to 46)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality Insert Length: 1695 Std Error: 0.00 Seg primer: -400P from Gibco High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2289346"
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Best Local Similarity 61.1
Matches 22; Conservative
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